

10/07

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RAW SEQUENCE LISTING

DATE: 10/08/2002

PATENT APPLICATION: US/10/024,494

TIME: 14:53:34

Input Set : N:\Crf3\RULE60\10024494.raw

Output Set: N:\CRF4\10082002\J024494.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: LI, YI

5 CAO, LIANG

6 ROSEN, CRAIG A.

8 (ii) TITLE OF INVENTION: Human GPR4 G-Protein Coupled Receptor and
9 Nucleotides Encoding Same (As Amended)

11 (iii) NUMBER OF SEQUENCES: 30

13 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

16 (B) STREET: 1100 NEW YORK AVE., NW, SUITE 600

17 (C) CITY: WASHINGTON

18 (D) STATE: DC

19 (E) COUNTRY: USA

20 (F) ZIP: 20005

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: FLOPPY DISK

24 (B) COMPUTER: IBM PC COMPATIBLE

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/024,494

C--> 30 (B) FILING DATE: 21-Dec-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/465,973

36 (B) FILING DATE: 06-JUN-1995

38 (A) APPLICATION NUMBER: PCT/US95/04079

39 (B) FILING DATE: 30-MAR-1995

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: STEFFE, ERIC K.

43 (B) REGISTRATION NUMBER: 36,688

44 (C) REFERENCE/DOCKET NUMBER: 1488.1140001/EKS/HCC

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: 202-371-2600

48 (B) TELEFAX: 202-371-2540

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1713 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: both

57 (D) TOPOLOGY: both

59 (ii) MOLECULE TYPE: cDNA

ENTERED

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62      (ix) FEATURE:
63          (A) NAME/KEY: CDS
64          (B) LOCATION: 116..1003
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 GGCACGAGGT CATTCAACAT TTATTCAACC AAAAATACTA AGTCAGCTCT ATACAAACTA      60
71 ATGGAAGGAT ACAGCTATGC AAATATAGAA CACTAAAGTG TTACATGACA GATGT ATG      118
72                                     Met
73                                     1
75 AGT AGT GAA ATG GTG AAA AAT CAG ACA ATG GTC ACA GAG TTC CTC CTA      166
76 Ser Ser Glu Met Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu
77           5                10                15
79 CTG GGA TTT CTC CTG GGC CCA AGG ATT CAG ATG CTC CTC TTT GGG CTC      214
80 Leu Gly Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu
81           20                25                30
83 TTC TCC CTG TTC TAT GTC TTC ACC CTG CTG GGG AAT GGG ACC ATC CTG      262
84 Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu
85           35                40                45
87 GGG CTC ATC TCA CTG GAC TCC AGA CTC CAC ACC CCC ATG TAC TTC TTC      310
88 Gly Leu Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe
89           50                55                60                65
91 CTC TCA CAC CTG GCC GTC AAC ATC GCC TAT GCC TGC AAC ACA GTG      358
92 Leu Ser His Leu Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val
93           70                75                80
95 CCC CAG ATG CTG GTG AAC CTC CTG CAT CCA GCC AAG CCC ATC TCC TTT      406
96 Pro Gln Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe
97           85                90                95
99 GCT GGT TGC ATG ACA CTA GAC TTT CTC TTT TTG AGT TTT GCA CAT ACT      454
100 Ala Gly Cys Met Thr Leu Asp Phe Leu Phe Leu Ser Phe Ala His Thr
101           100                105                110
103 GAA TGC CTC CTG TTG GTG CTG ATG TCC TAC GAT CGG TAC GTG GCC ATC      502
104 Glu Cys Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile
105           115                120                125
107 TGC CAC CCT CTC CGA TAT TTC ATC ATC ATG ACC TGG AAA GTC TGC ATC      550
108 Cys His Pro Leu Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile
109           130                135                140                145
111 ACT CTG GGC ATC ACT TCC TGG ACA TGT GGC TCC CTC CTG GCT ATG GTC      598
112 Thr Leu Gly Ile Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val
113           150                155                160
115 CAT GTG AGC CTC ATC CTA AGA CTG CCC TTT TGT GGG CCT CGT GAA ATC      646
116 His Val Ser Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile
117           165                170                175
119 AAC CAC TTC TTC TGT GAA ATC CTG TCT GTC CTC AGG CTG GCC TGT GCT      694
120 Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala
121           180                185                190
123 GAT ACC TGG CTC AAC CAG GTG GTC ATC TTT GAA GCC TGC ATG TTC ATC      742
124 Asp Thr Trp Leu Asn Gln Val Val Ile Phe Glu Ala Cys Met Phe Ile
125           195                200                205
127 CTG GTG GGA CCA CTC TGC CTG GTG CTG GTC TCC TAC TCA CAC ATC CTG      790
128 Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu

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129 210          215          220          225
131 GGG GGC ATC CTG AGG ATC CAG TCT GGG GAG GGC CGC AGA AAG GCC TTC      838
132 Gly Gly Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe
133          230          235          240
135 TCC ACC TGC TCC TCC CAC CTC TGC GTA GTG GGA CTC TTC TTT GGS AGC      886
136 Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser
137          245          250          255
139 GCC ATC GTC ATG TAC ATG GCC CCT AAG TCC CGC CAT CCT GAG GAG CAG      934
140 Ala Ile Val Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln
141          260          265          270
143 CAG AAG GTC CTT TTT CTT ATT TTA CAG TTC CTT TCA ACC CCG ATG CTT      982
144 Gln Lys Val Leu Phe Leu Ile Leu Gln Phe Leu Ser Thr Pro Met Leu
145          275          280          285
147 AAA CCC CCT GAT TTA CAA CCC TGA GGAATGTAGA GGGTCAAGGG TGCCCTCCGA      1036
148 Lys Pro Pro Asp Leu Gln Pro
149 290          295
151 GGAGACCACT GTGCAARGRA AGTCATTCCT AAGGGGTGTG ACATTTGAAC TGCCAGCCCC      1096
153 AGTTGCCCCG TGGACTCCTG ATGCCCAATT ATTGCCTCAA CCCAGAAAAG TTTACTCCCC      1156
155 TTTAACTGTG CTTTACTGAC AGAAGGGCAA GCCTTCTCCC GTTTTTTGCA GATAAAATTT      1216
157 TAGATGTGTT GCAATCATTG GGTTTCTAGG AGATGTGGTT TTATCAGACA ATTTTTCCTT      1276
159 TTATTTTACA ATTACTTTAA TATCTGTAAA ATAAAGAATT ATTTTAAATC ATTTTCCCAG      1336
161 TCCCAAAAGT TAAATACAGG CCACTTACTT CTTTAACCAA ATGATATAGT TTGGCTCTGT      1396
163 GTCCCCACCC AAATCTCATG TCAAATTGTA ATCCCCGCAT GTCAGCGGAG GGACCTGGTG      1456
165 GGAGGTGATT GGATCATGGG GAGGGATTTT CCCCTTGCTG TTCTGTTGAT AGTGAACGAG      1516
167 TTCTCACGAA ATCTGATGGT TTAAGAGTGC AGCACTTCTC CCTTTGCTCT CTCTCTCCTG      1576
169 CTGTGCCATG GTAAGACGTG CCTTGCTTCC CCTGGTGCTT CCGCCATGAT TGTACCTTTC      1636
171 CTGAGGCCCTC TCCAGCCATG TGGAACTGTG AGCCAATTAA ACTTCTTTTC TTTAGAAAAA      1696
173 AAAAAAAAAA AAAAAA      1713
176 (2) INFORMATION FOR SEQ ID NO: 2:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 296 amino acids
179 (B) TYPE: amino acid
180 (D) TOPOLOGY: linear
181 (ii) MOLECULE TYPE: protein
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
187 Met Ser Ser Glu Met Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu
188 1 5 10 15
190 Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly
191 20 25 30
193 Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile
194 35 40 45
196 Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe
197 50 55 60
199 Phe Leu Ser His Leu Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr
200 65 70 75 80
202 Val Pro Gln Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser
203 85 90 95
205 Phe Ala Gly Cys Met Thr Leu Asp Phe Leu Phe Leu Ser Phe Ala His
206 100 105 110

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208 Thr Glu Cys Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala
209          115          120          125
211 Ile Cys His Pro Leu Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys
212          130          135          140
214 Ile Thr Leu Gly Ile Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met
215 145          150          155          160
217 Val His Val Ser Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu
218          165          170          175
220 Ile Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys
221          180          185          190
223 Ala Asp Thr Trp Leu Asn Gln Val Val Ile Phe Glu Ala Cys Met Phe
224          195          200          205
226 Ile Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile
227          210          215          220
229 Leu Gly Gly Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala
230 225          230          235          240
232 Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly
233          245          250          255
235 Ser Ala Ile Val Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu
236          260          265          270
238 Gln Gln Lys Val Leu Phe Leu Ile Leu Gln Phe Leu Ser Thr Pro Met
239          275          280          285
241 Leu Lys Pro Pro Asp Leu Gln Pro
242          290          295
244 (2) INFORMATION FOR SEQ ID NO: 3:
246     (i) SEQUENCE CHARACTERISTICS:
247         (A) LENGTH: 2185 base pairs
248         (B) TYPE: nucleic acid
249         (C) STRANDEDNESS: both
250         (D) TOPOLOGY: both
252     (ii) MOLECULE TYPE: cDNA
255     (ix) FEATURE:
256         (A) NAME/KEY: CDS
257         (B) LOCATION: 884..2062
260     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
262 TCACTATAGG GCGAATTGGG TACGGGCCCC CCCTCGAGGT CGACGGTATC GATAAGCTTG      60
264 ATATCGAATT CGGCACGAGC CGGGCTCGGA GAGGTGACGG AACCGGGGCT GGTAGCATAG      120
266 TTTGATTTGA TGATGGAGCC AACACAGGGG TTGGAGCTGG TACCGGTGAA GCTGAGGCTA      180
268 AAAAGGTTCC TGGAGTAGAC GATGGAGCCA TAAGTGAAC CGGAGTCTGT GAATGAAGCC      240
270 AGGACAGGAG CAGCACCTGG CGATGGTGCC AGGACCGGAA GAGGAGCCAG AGGAGGAGCT      300
272 GGAGAAGGAG CCAGAATTGC TGTCTGTGGA GCCGCCATAG GAGCCAGAGG GGTGGCTAGA      360
274 GCCTGAGAAT GCAGAAGATG CTGGAGCCAG AAGGGAAGCC TGAGCTGGAG CTGGATTGAG      420
276 TGCTGACGGA AAAGGACTGG CCAGAGCCGA AGCTGGCACC AGGGACAGGT GAGCATTCTG      480
278 GGGCCACGGT TGAGTTCAAC CCACTGACTT CAGGTGAAGG ACTGTGGACC AGCTTGAGAA      540
280 GAGGCCACAC CAGAGTGGGT GTGGGGCATG GGGGCTCGAG CAGTACCCAG AGTAGGTGTG      600
282 GGTAGCCCGG CCAGGGGTTA ACGTGGGGCG TGGATTCAAC ACAGCTTGGA AGCCCAGAGC      660
284 TCGGAGGCCC GGGTGTCTGG GCCAATTGAG GAACAGGAGT CAGTCCATCC CGAGGGGGTT      720
286 GTCTCACTAC AATCTTCACA CGCCTTTATT ATTCACCATG GTTGGTGGCA CCTGGTTAGC      780
288 AGCAAGCGGA AGGCTGAGGC CAGTAGGGGC AGGGGTGTTA CTGGGGGTCG AAGAAGCCAG      840

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290	CACAGAGACA	GGGGTAGGGC	CAGGGGTCGG	GGCCACGGCC	TGG	ATG	AGG	CCC	ACA	895							
291						Met	Arg	Pro	Thr								
292						1											
294	TGG	GCA	GGC	TGG	CTG	ATG	AGA	TGG	TGC	TGC	CCC	CCT	GCT	GAC	ACG	AGG	943
295	Trp	Ala	Gly	Trp	Leu	Met	Arg	Trp	Cys	Cys	Pro	Pro	Ala	Asp	Thr	Arg	
296	5				10				15							20	
298	TGC	ACC	ACA	TTC	CTT	TGC	AGC	GGG	CGG	GCT	GCC	CCA	CAG	CAA	GCT	GGC	991
299	Cys	Thr	Thr	Phe	Leu	Cys	Ser	Gly	Arg	Ala	Ala	Pro	Gln	Gln	Ala	Gly	
300					25				30							35	
302	GCA	CCT	GGG	CAC	CAT	CCA	AAA	TAC	AGC	TTG	TTT	CCC	TGG	ATT	TGG	AAG	1039
303	Ala	Pro	Gly	His	His	Pro	Lys	Tyr	Ser	Leu	Phe	Pro	Trp	Ile	Trp	Lys	
304					40				45							50	
306	GTG	AGA	GGT	TTG	CTT	CCC	CCT	CCA	TTA	ACC	ACT	GAC	GTT	GTG	CCA	GTG	1087
307	Val	Arg	Gly	Leu	Leu	Pro	Pro	Pro	Leu	Thr	Thr	Asp	Val	Val	Pro	Val	
308					55				60							65	
310	AGA	CTA	ACT	CTC	CGC	GCC	AAT	CTG	TCC	GCG	GCT	GAC	CTC	CTT	CGC	GGG	1135
311	Arg	Leu	Thr	Leu	Arg	Ala	Asn	Leu	Ser	Ala	Ala	Asp	Leu	Leu	Arg	Gly	
312					70				75							80	
314	CGT	GGC	CTA	CCT	CTT	CCT	CAT	GTT	CCA	CAC	TGT	CCC	CGC	ACA	GCC	CGA	1183
315	Arg	Gly	Leu	Pro	Leu	Pro	His	Val	Pro	His	Cys	Pro	Arg	Thr	Ala	Arg	
316	85						90				95					100	
318	CTT	TCA	CTT	GAG	GGC	TGG	TTC	CTG	CGG	CAG	GGC	TTG	CTG	GAC	ACA	AAC	1231
319	Leu	Ser	Leu	Glu	Gly	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Thr	Asn	
320					105				110							115	
322	CTC	ACT	GCG	TCG	GTG	GCC	ACA	CTG	CTG	GCC	ATC	GCC	GTG	GAG	CGG	CAC	1279
323	Leu	Thr	Ala	Ser	Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala	Val	Glu	Arg	His	
324					120				125							130	
326	CGC	AGT	GTG	ATG	GCC	GTG	CAG	CTG	CAC	AGC	CGC	CTG	CCC	CGT	GGC	CGC	1327
327	Arg	Ser	Val	Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu	Pro	Arg	Gly	Arg	
328					135				140							145	
330	GTG	GTC	ATG	CTC	ATT	GTG	GGC	GTG	TGG	GTG	GCT	GCC	CTG	GGC	CTG	GGG	1375
331	Val	Val	Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	Leu	Gly	Leu	Gly	
332					150				155							160	
334	CTG	CTG	CCT	GCC	CAC	TCC	TGG	CAC	TGC	CTC	TGT	GCC	CTG	GAC	CGC	TCC	1423
335	Leu	Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala	Leu	Asp	Arg	Ser	
336	165						170				175					180	
338	TCA	CGC	ATG	GCA	CCC	CTG	CTC	AGC	CGC	TCC	TAT	TTG	GCC	GTC	TGG	GCT	1471
339	Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu	Ala	Val	Trp	Ala	
340					185				190							195	
342	CTG	TCG	AGC	CTG	CTT	GTC	TTC	CTG	CTC	ATG	GTG	GCT	GTG	TAC	ACC	CGC	1519
343	Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala	Val	Tyr	Thr	Arg	
344					200				205							210	
346	ATT	TTC	TTC	TAC	GTG	CGG	CGG	CGA	GTG	CAG	CGC	ATG	GCA	GAG	CAT	GTC	1567
347	Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met	Ala	Glu	His	Val	
348					215				220							225	
350	AGC	TGC	CAC	CCC	CGC	TAC	CGA	GAG	ACC	ACG	CTC	AGC	CTG	GTC	AAG	ACT	1615
351	Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser	Leu	Val	Lys	Thr	
352					230				235							240	
354	GTT	GTC	ATC	ATC	CTG	GGG	GCG	TTC	GTG	GTC	TGC	TGG	ACA	CCA	GGC	CAG	1663

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10024494.raw

Output Set: N:\CRF4\10082002\J024494.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:872 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:884 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:896 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:908 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:921 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:933 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:945 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:957 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:969 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:992 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:1004 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:1016 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:1028 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:1041 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:1053 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1066 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1091 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:1148 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:1235 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29
L:1313 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30